DAARTSHALL 435 69.

## 1/3 Interleukin-20

1					T	'CCA	.GG(	:GGG	CAG	CAG	CTG	CAG	GCT	GAC	CTT	'GCA	.GCT	TGG	CGG	AΑ	.45:
1								:												<u>M</u>	1
46	TGGA	.CTG	GCC	TCA	.CAA	CCT	· GCI	GTT	TCT	TCT	TAC	CAT	· TTC:	CAT	CTT	CCT	· 'GGG	GCT	GGG	ICC	105
2	D	W	P	Н	N	L	L	F	L	L	T	Ι	S	Ι	F	L	G	L	G	Q	21
			*.	-		*															
106	AGCC	CAG	GAG	CCC	CAA	AAG	CAA	GAG	GAA	GGG	GCA	AGG	GCG	GCC	'TGG	GCC	CCT	'GGC	CCC	TG	165
22	P	R	S	P	K	S	K	R	K	G	Q	G	R	P	G	P	L	A	P	G	41
166	GCCC	TCA	CCA	.GGT	'GCC	'ACT	· 'GG <i>I</i>	CCT	GGT	GTC	ACG	GAT	· GAA	ACC	GTA	TGC	!CCG	CAT	GGA	.GG	225
42	Р	Н	Q	V	P	L	D	L	V	S	R	M	K	Р	Y	Α	R	M	Ε	Ε	61
														#							
226	AGTA	TGA	.GAG	GAA	CAT	'CGA	.GG <i>I</i>	GAT	GGT	GGC	CCA	.GCT	'GAG	GAA	CAG	CTC	'AGA	.GCT	GGC	CC.	285
62	Y	E	R	N	Ι	E	E	M	V	Α	Q	L	R	N	S	S	E	L	Α	Q	81
										•		*									
286	AGAG	AAA	.GTG	TGA	.GGT	'CAA	CT7	GCA	GCT	GTG	GAT	'GTC	CAA	CAA	GAG	GAG	CCT	'GTC	TCC	CT	345
82	R	K	С	E	V	N	L	Q	L	W	M	S	N	K	R	S	L	S	P	W	101
								CD-	I										C	D-I	I
346	GGGG	СТА	CAG	CAT	'CAA	CCA	.CGI	CCC	CAG	CCG	TAT	'CCC	CGT	'GGA	CCT	'GCC	'GGA	.GGC	ACG	GT	405
102	G	Y	S	<u>I</u>	N	Н	D	Р	S	R	Ι	<u>P</u>	V	D	L	Р	E	Α	R	<u>C</u>	121
		C	D-1	ī						*										-	
406	GCCT	'GTG	TCT	'GGG	CTG	TGT	'GA <i>I</i>	CCC	CTT	CAC	CAT	'GCA	GGA	GGA	.CCG	CAG	CAT	'GGT	GAG	CG	465
122	L	С	L	G	<u>C</u>	V	N	Р	F	T	M	Q	E	D	R	S	M	V	S	V	141
	•							C													
466	TGCC	GGT	GTT	'CAG	CCA	GGT	TCC	TGT	'GCG	CCG	CCG	CCT	'CTG	CCC	:GCC	ACC	:GCC	CCG	CAC	AG	525
142	P	V	F	S	Q	<u>V</u> _	Р	V	R	R	R	_ <u>L</u>	С	Р	P	P	P	R	T	G	161
														CL							
526	GGCC	TTG	CCG	CCA	.GCG	CGC	'AG'I	CAT	'GGA	GAC	CAT	'CGC	TGT	'GGG	CTG	CAC	CTG	CAT	CTT	СТ	585
162	P	С	R	Q	R	A	V	M	E	T	I	Α	V	G	С	T	С	Ι	F	*	180
586	GAAT	'TAC	CTC	GCC	CAG	AAG	CCI	\GGC	'CAG	CAG	CCC	'GAG	ACC	'ATC	CTC	CTT	'GCA	CCT	TTG	TG	645
646	CCAA	GAA	AGG	CCT	'ATG	AAA	AG1	'AAA'	CAC	TGA	CTT	TTG	AAA	GCA	AAA	AAA	AAA	AAA	AAA	AA	705

FIG. 1

uss 69.

IL20.aa x IL17.aa

	·	
1	${\tt MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGQGRPGPLAPGPHQVPLD}$	48
	:  .:. ::  :.   .  :::	
5	KTSLVSLLLLLSLEAIVKAGITIPRNPGCPNSED	38
49	LVSRMKPYARMEEYERNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSL	98
39	KNFPRTVMVNLNIHNRNTNTNPKRSSDYYNRST	71
	•	
99	SPWGYSINHDPSRIPVDLPEARCLCLGCVNPFTMQEDRSMVSVPVFSQVP	148
72	SPWNLHRNEDPERYPSVIWEAKCRHLGCINA.DGNVDYHMNSVPIQQEIL	120
149	VRRRLCPPPPRTGPCRQRAVMETIAVGCTCI 179	
121	VLRREPPHCPNSFRLEKILVSVGCTCV 147	

FIG. 2



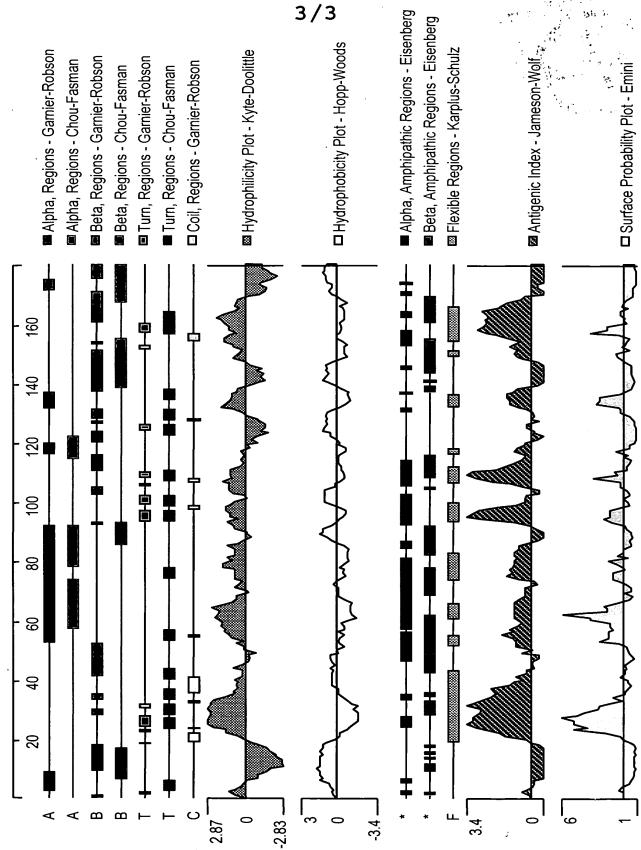


FIG. 3